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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

October 17, 2003, 09:21:39; Search time 237 Seconds Run on:

(without alignments) 10249.656 Million cell updates/sec

US-10-039-836A-3

1 actatagggcacgcgtggtc........0cgcaggaaggaaatctatc 925 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1750203 seqs, 1313063994 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Published_Applications_NA:*

Database :

/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/PCUS_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/PCUS_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US08_NEW_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*/cgn2_6/ /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID 925 100.0 925 14 US-10-039-836A-3 59.6 6.4 925 14 US-10-039-836A-3 44 4.7 95.2 14 US-10-039-836A-3 42.6 4.6 10328 12 US-10-311-841-2 42.6 4.6 18917 12 US-10-311-455-1138 42.2 4.6 10254 12 US-10-311-455-1048 42.4 4.5 17594 12 US-10-311-455-1099 41.4 4.5 17594 12 US-10-311-455-1399 41.4 4.5 17594 12 US-10-311-455-1399 41.4 4.5 17594 12 US-10-311-455-1399 41 4.4 5488 12 US-10-311-455-1368 40.8 4.4 2000 10 US-00-938-842A-5309 40.6 4.4 5487 12 US-10-311-455-1309	Sequence 85, Appl
Query Match Length DB 100.0 925 14 5.0 10328 12 4.8 363778 12 4.6 10524 12 4.6 10517 12 4.5 10594 12 4.5 10594 12 4.5 10594 12 4.4 5488 12 4.4 5488 12 4.4 2006 12 4.4 288 12 4.4 288 12 4.4 288 12	US-10-311-455-85
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Sequence 272, App Sequence 996, App Sequence 1, Appli Sequence 14, Appli Sequence 14, Appli Sequence 1214, Appli Sequence 21, Appli Sequence 23, Appli Sequence 23, Appli Sequence 1, Appli Sequence 1030, Appli Sequence 1030, Appli Sequence 1, Appli Sequence 1030, Appli Sequence 1685, Appli Sequence 1685, Appli Sequence 1686, Appli Sequence 1685, A	acuenbes acuenbes acuenbes acuenbes acuenbes acuenbes acuenbes acuenbes acuenbes acuenbes
US-10-311-455-272 US-10-311-455-996 US-10-312-841-1 US-10-312-841-2 US-10-313-841-2 US-10-311-455-1822 US-10-311-455-2214 US-10-311-455-2214 US-10-268-794-23 US-10-268-794-23 US-10-312-841-1	US-10-027-632-186112 US-10-311-455-575 US-10-311-455-575 US-10-184-385-5 US-10-184-385-6794 US-10-312-585-6794 US-10-314-455-690 US-10-311-455-1128 US-10-311-455-811
12507 12 16336 12 3673778 12 763 14 7057 12 7057 12 11691 12 11691 12 1734 14 1734 14 1734 14 1734 14 1734 12 160681 10 3673778 12 49 14 18 13 18 13 18 13 18 13	615 13 5912 12 18218 12 1172 12 7676 12 7676 12 5807 12 9524 12
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ALIGNMENTS

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1 ACTATAGGGCACGCGGGCGACGCCCGGGCTGGTCGTATTGTGTCCAAACATTTGG 60
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                                                                                   APPLICANT: Crandon, Virginia
APPLICANT: Crandon, Virginia
TILE OF INVENTION: Maize Proteinase Inhibitor-Like
TILLE OF INVENTION: Maize Proteinase Inhibitor-Like
TILLE REFERENCE: 35718/239836
CURRENT APPLICATION NUMBER: US/10/039,836A
CURRENT PILING DATE: 2001-10-23
PRIOR PRIOR APPLICATION NUMBER: 60/243,167
PRIOR PRIOR APPLICATION NUMBER: 60/243,167
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Proteinase Inhibitor-like promoter
US-10-039-836a-3
            Sequence 3, Application US/10039836A; Publication No. US20030033632A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3
US-10-039-836A-3
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                           301 AAAATTGTTAGTGAAATTATCTAGCTAACAAATAGCTACCTAACTATTAACTAATTTACC
                                                                                                                                                                                                     361 AAAAATAACTTATAGTTAAATTATTAAGTTGGGCTGTTTGAATGTCTCAACTAATTTTAG
                                                                                                                                                                                                                               361 AAAAATAACTTATAGTTAAATTATTAAGTTGGGCTGTTTGAATGTCTCAACTAATTTTAG
                                                                                                                                                                                                                                                         421 CCACTAACTTTTATCTTTAGTGCATTCAAACATGGCATAAGTCTACGTTTGATTTGAGAC
                                                                                                                                                                                                                                                                       GGTAGCATCGTGCGTACGGAAGAGGAACCAAAAGGATTTTCCTTGAAAATTTTCATGCAC
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APPLICANT: Simmons, Carl
TITLE OF INVENTION: Maize Proteinase Inhibitor-Like
TITLE OF INVENTION: Maize Proteinase Inhibitor-Like
TITLE OF INVENTION: Polynucleotides and Methods of Use
FILE REFERENCE: 35718/239836
CURRENT APPLICATION NUMBER: US/10/039,836A
CURRENT FILING DATE: 2001-10-23
PRIOR FILING DATE: 2000-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-039-836A-3/c
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Sequence 1518, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITTLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by II
FILE REPERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT PILING DATE: 2002-12-16
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                                                                                                                                                                                                                                                                   303 AATTGTTAGTGAAATTATCTAGCTAACAAATAGCTACCTAACTATTAACTAATTTACCAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                   363 AAATAACITATAGITAAAITAITAAGITGGGCIGITIGAAIGICTCAACTAAITITAGCC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 AATTAGTTAATAGTTAGGTAGCTATTTGTTAGCTAGATAATTTCACTAACAATTTTAGCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1518
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                                                                                                                                                                                   6.4%; Score 59.6; DB 14; Length 925;
59.0%; Pred. No. 4.5e-05;
Live 0; Mismatches 94; Indels 2
                                                                    NAME/KEY: misc_feature
LOCATION: (0)...(0)
COLORY INFORMATION: Proteinase Inhibitor-like promoter
US-10-039-836A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.0%; Score 45.8; DB 12;
46.2%; Pred. No. 0.55;
tive 0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PELICATION NUMBER: DE 10043529.7
PRIOR PELICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                     Best Local Similarity 59.09
Matches 138; Conservative
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               TYPE: DNA
ORGANISM: Zea mays
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US-10-311-455-1518
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LENGIH:
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                                                                                                                                                                                                                                                                                                                                                   189 ATTITCTICITIGICGCACIGITICIACAITICATIGGCAGAIAIGIATGAACIAAAFIA
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                                                                                                                                                                                                                                                                                                         Gaps
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REPERENCE: 5013.1007
CURRENT APPLICATION UNMBER: US/10/240,485
CURRENT FILING DATE: 2002-10-02
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PRIOR POSTION NUMBER: DE 10013529.7
PRIOR PRIOR POSTION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 202
                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                    Score 43.6; DB 12;
Pred. No. 1.9;
0; Mismatches 154;
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ularity 48.2%; Pred. No. 5;
Conservative 0; Mismatches 129;
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Publication No. US20030148327A1
GENERAL INFORMATION:
                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                    Query Match 4.7%;
Best Local Similarity 46.9%;
Matches 136; Conservative
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Best Local Similarity
Matches 120; Conserv
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SEQ ID NO 812
LENGTH: 9524
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                                                                                                                        FEATURE:
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Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

ITILE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.101

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SEQUENCE:
GENERAL SEQUENCE:
GENERAL SEQUENCE:
GENERAL SEQUENCE:
GENERAL SEQUENCE:
GURRENT APPLICATION UNDER:
UNDER:
GURRENT FILING DATE:
2002-12-30
UNDER:
ON OF SEQUENCE:
GENERAL SEQ
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                                                                                                                                    432 TATCTTTAGTGCATTCAAACATGGCATAAGTCTACGTTTGATTTGAGACGGTAGCATCGT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 ACATITCATIGGCAGATAIGTATGAACTAAAITATIGGCCACTIAAGGAGGIGTTIGAAT 274
                     372 ATAGTTAAATTATAAGTTGGGCTGTTTGAATGTCTCAACTAATTTTAGCCACTAACTTT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 GCAATAAAACTAATAGTTAGTTGGCTAAAATTGTTAGTGAAATTATCTAGCTAACAAATA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 12; Length 36
Pred. No. 33;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                          2521 TCGAATTTATAAGGATTTTAAATAATTGT 2549
                                                                                                                                                                                                                                                      492 GCGTACGGAAGAACCAAAAGGATTTT 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 3673778
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US-10-312-841-2/c
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Best Local S:
Matches 92
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rullication no. uszuojajabohal
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1999
LENGTH: 17594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 TTAACTAATTTACCAAAAATAACTTATAGTTAAATTATTAAGTTGGGCTGTTTGAATGTC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-485-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.5%; Score 41.6; DB 12; Length 7676;
Best Local Similarity 53.8%; Pred. No. 5.6;
Matches 86; Conservative 0; Mismatches 74; Indels 0;
                                                                 Sequence 152, Application US/10240485
Publication No. US20030148327A1
GENERAL INFORMATION:
APPLICANT: OLEX, Alexander:
APPLICANT: DLEY, Alexander:
APPLICANT: DLEY, Alexander:
APPLICANT: DLEY, Alexander:
APPLICANT: DLEY, Alexander:
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE OF INVENTION: Metastasis
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT APPLICATION NUMBER: CT/FE01/03970
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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Publication No. US20030143606A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 152
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; Publication No. US2003014366A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIERLIN, Kurt
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: DCT/FP01/07537
PRIOR PILING DATE: 2000-06-30
; PRIOR PILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
                                                     12872 AAAAAAAAACACATATTAAATAAAAAAAATAAATACTATTCAACTCTCACCAAAAA 12813
                                                                                                                                          3285 GGTATATTTGAAAAGATAAAAATGTATGTTAATGAAATGATTAAATTATATATATAAAAT 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AGTIAGTIGGCTAAAATIGTIAGTGAAATTATCTAGCTAACAAATAGCTACCTAACTAIT 348
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278 ATAAAACTAATAGTTGGCTAAAATTGTTAGTGAAATTATCTAGCTAACAAATAGCT 337
                                                                                                        338 ACCTAACTATTAACTAATTTACCAAAATAACTTATAGTTAAATTATTAAGTTGGGCTGT 397
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48.2%; Pred. No. 4.6;
tive 0; Mismatches 128; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 5274, 6551, 9520
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-1048
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8525 TTTATT 8531
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APPLICANT: OLEK, Alexander
APPLICANT: DLEK, Alexander
APPLICANT: DLEK, Alexander
APPLICANT: DEFENBROCK, Christian
APPLICANT: DEFENBROCK, Christian
APPLICANT: DLEK, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by De
ITILE OF INVENTION: Cytosine methylation
FILE REPERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2000-70-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR PELICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1429
LENGTH: 5488
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Sequence 1368 Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: DIEENBROCK, Christian

APPLICANT: DISPERBROCK, Christian

APPLICANT: DIAGNOSIS of Diseases Associated with the Immune System by DF:

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/FP01/07537

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 AAATIGITAGIGAAATTAICTAGCIAACAAATAGCIACCIAACIATTAACTAATTIACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAATAACTTATAGTTAAATTATTAAGTTGGGCTGTTTGAATGTCTCAACTAATTTTAGC
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.4%; Score 41; DB 12; Length 5488;
Best Local Similarity 55.2%; Pred. No. 6.8;
Matches 80; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 12;
Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 CACTAACTTTTATCTTTAGTGCATT 446
    Sequence 1429, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: OLEK, Alexander
APPLICANT: DLEEN, Alexander
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
FILE REFRENCE: 5013.1014
FILE REFRENCE: 2001-12-16
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PRICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 524
LENGTH: 6275
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                                                                                                                                                                                                                                                                                                                                                                                                                                     212 TCTACATTTCATTGGCAGATATGTATGAACTAAATTATTGGCCACTTAAGGAGGTGTTTG 271
                                                                                                                                                                                                                                            332 ATAGC-TACCTAACTATTAACTAATTTACCAAAATAACTTATAGTTAAATTATTAAGTT 390
                                                                                                                                                                                                                                                                                                          272 AATGCAATAAAACTAATAGTTAGTTGGCTAAAATTGTTAGTGAAATTATCTAGCTAACAA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 CCTAACTATTAACTAATTTACCAAAATAACTTATAGTTAAATTATTAAGTTGGGCTGTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 TAAAAACTAATAGTTAGTTGGCTAAAATTGTTAGTGAAATTATCTAGCTAACAAATAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 GGGCTGTTTGAATGTCTCAACTAATTTTAGCCACTAACTTTTATCTTTAGT 441
                           ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1999
                                                                                                                        Length 17594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-524
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4.5%; Score 41.2; DB 12; Length 6275;
Best Local Similarity 52.3%; Pred. No. 6.4;
Matches 91; Conservative 0; Mismatches 83; Indels 0;
                                                                                                                 Query Match

4.5%; Score 41.4; DB 12; Length
Best Local Similarity 51.5%; Pred. No. 9.8;
Matches 119; Conservative 0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-311-455-524/c
. Sequence 524, Application US/10311455
. Publication No. US20030143606A1
. GENERAL INFORMATION:
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-311-455-1429
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Length 5930;

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Sequence 157.1, Application US/10311455
; Bouldance 157.1, Application US/10311455
; Bublication No. US20030143606A1
; GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by D:
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by D:
TITLE OF INVENTION: USUALS: US/10/311,455
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2000-12-16
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1571
                                                                                                                                                                                                                                                                                                                                                                                                                      334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 GCTACCTAACTATTAACTAATTTACCAAAATAACTTATAGTTAAATTATTAAGTTGGGC 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 GCAATAAAACTAATAGTTAGTTGGCTAAAATTGTTAGTGAAATTATCTAGCTAACAAATA
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                                                                                                                                                                                                                                                                           Length 2000;
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                                                                                                                                                                                                                                                                                                                               94;
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4.4%; Score 40.6; DB 12;
Best Local Similarity 56.3%; Pred. No. 8.6;
Matches 76; Conservative 0; Mismatches 59;
                                                                                                                                                                                                                                                                     4.4%; Score 40.6; DI 50.8%; Pred. No. 5.1; tive 0; Mismatches
                    60/300,111
                                                                                                                                                    TYPE: DNA
CORGANISM: Arabidopsis thaliana
US-09-938-842A-5309
        PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5309
LENGTH: 2000
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Best Local Similarity 50.89
Matches 97; Conservative
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1548 TATTTGATTCT 1538
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Sequence 5309, Application US/09938842A
Sequence 5309, Application US/09938842A
Settle Thrormathron:
Sequence 5309, Application US/09938842A
Settle Thrormathron:
Sequence 5309, Application
Sequence
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APPLICANT: Grasso, Luigi
APPLICANT: Grasso, Luigi
APPLICANT: Sasso, Luigi
APPLICANT: Sasso, Philip M.
APPLICANT: Sasso, Philip M.
APPLICANT: Nicolaides, Nicholas C.
TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagnosi
FILE REFRENCE: AGOOGUSG (MOR-0133)
CURRENT APPLICATION NUMBER: US/10/270,839
FRIOR APPLICATION NUMBER: 60/328,750
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
LENGTH: 88
                                                                                                           5093 AAATTTAAAAACTAAAATTCCTAAAATCTAAATTATTAACTATAAAATAAAAA 5034
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                                                    230 ATATGTATGAACTAAATTATTGGCCACTTAAGGAGGTGTTTGAATGCAATAAAACTAATA 289
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           Gaps
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           Indels
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        Mismatches 105;
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Pred. No. 0.88;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                  410 ACTAATTTTAGCCACTAACTTTTATCTTT 438
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; Publication No. US20030143586A1
; GENERAL INFORMATION:
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l Similarity 75.0%;
51; Conservative (
Matches 104; Conservative
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28 TCAGATCG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Conyza sp.
US-10-270-839-108
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US-09-938-842A-5309/c
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Best Local S:
Matches 51,
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LOCATION:
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US-08-750-357-7
Sequence 14, Apprasequence 3328, Apsequence 1, Appli
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Sequence 36, Appl
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 36, 3
Sequence 1, 3
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1 actatagggcacgcgtggtc......ccgcaggaaggaaatctatc
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Sequence
Sequence
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcaycomB.seq:*
               GenCore version 5.1.6
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US-09-313-294A-7567
US-09-313-294A-3567
US-08-750-357-7
US-09-276-599-14
US-09-313-294A-3328
US-09-313-294A-3328
US-09-313-914-1
US-09-313-914-1
US-09-98-046-5
US-09-601-198-3
US-09-601-108-3
US-09-601-108-3
US-09-601-108-3
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US-07-991-867B-23
US-08-107-55A-23
US-08-544-332-23
US-09-424-283-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          569978 seqs, 220691566 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WILLIAMS, Mark
APPLICANT: WILLIAMS, Mark
APPLICANT: LEEMANS, Jan
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
COUMTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: ECORI-HindIII region of plasmid pCOL13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: #PPLICATION NUMBER: US/08/750,357 FILING DATE: 21-MAR-1997 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                             US-07-991-867B-1
US-08-544-332-1
US-09-307-861A-1
US-09-402-532-38
US-09-402-532-38
US-08-545-528D-1
US-08-942-532-1
US-08-943-1
US-09-257-583-5
US-09-377-644-4
US-09-383-543A-4
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US-09-004-056-1
US-09-570-367C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MCGOWAN, MAICOLM K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 018030-100
TELECOMMUNICATION INPORMATION:
TELEFRONE: (703) 836-6620
TELEFAX: (703) 836-6201
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08750357
Patent No. 6008437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prim_transcript
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US-09-313-294A-7567/c

Sequence 7567, Application US/09313294A

Sequence 7567, Application US/09313294A

Patent No. 6476212

GENERAL INFORMATION: Laura Y.

APPLICANT: Lalqudi, Raghunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US

CURRENT APPLICANTION NUMBER: US/09/313, 294A

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                    262 GAGGTGTTTGAATGCAATAAAACTAATAGTTAGTT-AAAATTGTTAGTGAAATTA 319
                                                                                                                                                                                                                                                                                                                       320 TCTAGCTAACAAATAGCTACCTAACTATTAACTAATTTACCAAAAATAACTTATAGTTAA 379
                                                                                                                                                                                                                                                                                                                                                                                            380 ATTATTAAGTTGGGCTGTTTGAATGTCTCAACTAATTTTAGCCACTAACTTTTATCTTTA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 TAAGGAGGTGTTTGAATGCAATAAAACTAATAGTTAGTTGGCT-AAAATTGTTAGTGAAA 316
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CTHER INFORMATION: Incyte ID No. 6476212 700381949H1

NAME/KEY: unsure

LOCATION: 101, 104, 234, 255, 258, 268, 280, 285-286, 289, 297, 314

COTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-7567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 GIGCATICAAACAIGGCATAAGICIACGITIGAITIGAGACGGIAGCAIC 489
                                                                                                                                                                             Query Match 10.9%; Score 100.8; DB 3; Length 4137; Best Local Similarity 67.8%; Pred. No. 8.8e-19; Matches 156; Conservative 0; Mismatches 72; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 99; DB 4; Length 318; 84.7%; Pred. No. 1.1e-18; tive 0; Mismatches 21; Indels
                                                                                       ; OTHER INFORMATION: /label- polylinker
; OTHER INFORMATION: /note= "part of polylinker of pUC19"
US-08-750-357-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 TAAATTATTAAGTTGGGCTGTTTG 400
                 LOCATION: 4132..4137
OTHER INFORMATION: /label= HindIII
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Best Local Similarity 84.74
Matches 122; Conservative
               4132..4137
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NAME/KEY:
                                                                      NAME/KEY:
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                                                                                                                                                                                            OTHER INFORMATION: /codon_start= 2 OTHER INFORMATION: /note= "exon containing 3' end coding region of B-peru gene. OTHER INFORMATION: This exon continues up to the polyadenylation site."
                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "fragment of B-peru coding OTHER INFORMATION: region which is derived from cDNA'
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LOCATION: 265..270
OTHER INFORMATION: /label= HindIII
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LOCATION: 2788..2793
OTHER INFORMATION: /label= HindIll
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OTHER INFORMATION: /label= ECORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /label- BamHl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 4114..4119
OTHER INFORMATION: /label= SalI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 45..50
OTHER INFORMATION: /label= KpnI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 329..334
OTHER INFORMATION: /label= xbal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1269..1274
OTHER INFORMATION: /label= MluI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /label= Mun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: - 2828..2833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATURE.
NAME/KEY: - 2884..2889
                                                                                                                                                                                                                                                                                                                     CDS
1226..2771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3'UTR
2772..4137
                                                                                                                                                                                                                                                                                                                                                                                              1269..2771
                                                                                                                                                                              .226 . . 2771
                                                                                                                         719..1224
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576..718
                                                       exon
557..718
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               213..556
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OTHER INFORMATION:
                                                                                                        intron
                                                                                                                                                                 exon
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                                                   NAME/KEY:
LOCATION:
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NAME/KEY:
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NAME, N.L.

LOCATION: 719..1zz.

FEATURE:
NAME/KEY: exon
LOCATION: 1226..2771
OTHER INFORMATION: /codon_start= 2
OTHER INFORMATION: /codon_start= 2
OTHER INFORMATION: /note= "exon containing 3' end coding region of B-peru ge."

OTHER INFORMATION: /note= "exon continues up to the polyadenylation site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "fragment of B-peru coding region which is derived from cDNA"
                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
COMPURY: United States
ZIP: 22313-1404
COMPURER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/750,357

FILING DATE: 21-MAR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: MGGMAN, MAIOOIM K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 018030-100

TELEPHONE: (703) 836-620

TELEPHONE: (703) 836-2021

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 4137 base pairs

TYPE: nucleic acid

STRANDENDESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECORI-HindII region of plasmid pCOL13
TITLE OF INVENTION: MALE STERILE PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 1.6
OTHER INFORMATION: /label= ECORI
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prim_transcript
188
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1226..2771
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LOCATION: 1269..2771
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557..718
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188..212
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OTHER INFORMATION:
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NAME/KEY: 3'UTR
LOCATION: 2772...
FEATURE:
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LOCATION:
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LOCATION:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2899 TTAATAAATTTAATAAAAATATGTTAAATTTAAATTAAATGTTAAATTAAACTTAAATT 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 TTATCTAGCTAACAAATAGCTACTAACTATTAACTAATTTACCAAAAATAACTTATAGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 TAAATTATTAAGTTGGGCTGTTTGAATGTCTCAACTAATTTTAGCCACTAACTTTTATCT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Best Local Similarity 53.0%; Pred. No. 0.0038;
Matches 97; Conservative 0; Mismatches 86; Indels 0
                                     US-07-872-678A-36/C

Sequence 36, Application US/07872678A

Patent No. 5541060

GENERAL INFORMATION:
APPLICANT: Bell, Graeme, et al.
TITLE OF INVENTION: DETECTION OF EARLY-ONSET
TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELLITUS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-750-357-7/C
Sequence 7, Application US/08750357
Patent No. 6008437
GENERAL INFORMATION:
APPLICANT: KREBBERS, Enno
APPLICANT: WILLIAMS, Mark
APPLICANT: LEBRANS, Jan
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,678A
FILING DATE: 22-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFENCE/DOCKET NUMBER: ARCD016
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold, White & Durkee STREET: Post Office Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLE...
TELERAX: 713-702 TELERAX: 79-0924
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS: LENGTH: 3618 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPE: Nucleic Acid STRANDEDNESS: Single TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2779 ATA 2777
                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas
COUNTRY: USA
ZIP: 77210
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TYPE: DNA
ORGANISM: Zea mays
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LOCATION: 266
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US-09-276-599-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269
                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 TAAGGAGGTGTTTGAATGCAATAAAACTAATAGTTAGTTGGCTAAAATTGTTAGTGAAAT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 TATCTAGCTAACAAATAGCTACCTAACTATTAACTAATTTACCAAAAATAACTTATAGTT 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.4%; Score 40.8; DB 3; Length 4137; 56.2%; Pred. No. 0.08; Itive 0; Mismatches 87; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COTHER INFORMATION: /label- polylinker OTHER INFORMATION: /note- "part of polylinker of pucl9" US-08-750-357-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3353 TTCAAGTACATTTAAACACCTCTAAATT 3326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -
LOCATION: 2828..2833
OTHER INFORMATION: /label= HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: -
LOCATION: 2788..2793
OTHER INFORMATION: /label= HindIII
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                                                                                                                                                                                     OTHER INFORMATION: /label= Hindill
                                                                                                                                                                                                                                                                                                     LOCATION: 835..840
OTHER INFORMATION: /label= BamHI
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OTHER INFORMATION: /label= Sali
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
LOCATION: 1269..1274
OTHER INFORMATION: /label= Mlul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 2884..2889
OTHER INFORMATION: /label= MunI
                                                                                                                                                                                                                                      LOCATION: 329..334
OTHER INFORMATION: /label= xbaI
               NAME/KEY: -
LOCATION: 11..16
OTHER INFORMATION: /label= XbaI
                                                                                                                 OTHER INFORMATION: /label= KpnI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 117; Conservative
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                                                                                                                                                                 265..270
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Best Local Similarity
                                                                                 NAME/KEY: -
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RESULT 5

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Sequence 3328, Application US/09313294A
Patent NO. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNOCEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 UG
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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4.3%; Score 39.6; DB 4; Length 269;
Best Local Similarity 83.6%; Pred. No. 0.061;
Matches 56; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.4%; Score 40.4; DB 4; Length 763; 97.6%; Pred. No. 0.054; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        759 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCTTT 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCGTATT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700611343H1
                                                                            APPLICANT: Perera, J. Ranjan
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Composition and methods for the
TITLE OF INVENTION: modification of gene expression
FILE REFERENCE: 11000.1036
CURRENT APPLICATION NUMBER: US/09/276,599
CURRENT APPLICATION DATE: 1999-03-25
NUMBER OF EQU ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: a, t, c, g, or other US-09-313-294A-3328
Sequence 14, Application US/09276599 Patent No. 6380459 GENERAL INFORMATION:
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Sequence 1, Application US/09173914

Partent No. 6171857

; GENERAL INFORMATION:

APPLICANT: Hendrickson, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pinus radiata
US-09-276-599-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 GCTAACA 330
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297 GGCTAAAATTGTTAGTGAAATTATCTAGCTAACAAATAGCTACCTAACTATTAACTAATT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wohr, Christine
APPLICANI: Wohr, Christine
APPLICANI: Mendland, Jurgen
APPLICANI: Knechtle, Philipp
APPLICANI: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 62222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.2%; Score 39; DB 3; Length 615; 50.8%; Pred. No. 0.12; Live 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38.241
REFERENCE/DOCKET NUMBER: 9F/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                   Sequence 186, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 50.8
Matches 93; Conservative
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                                                                                                                        GENERAL INFORMATION:
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MOLECULE TYPE: DN
ORIGINAL SOURCE:
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                                              RESULT 9
US-08-998-416-186
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TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
FILE REFERENCE: B087/77017/HK
CURRENT APPLICATION NUMBER: US/09/173,914
CURRENT FILING DATE: 1998-10-16
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSED for Windows Version 3.0
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APPLICANT: Pullman, Gerald
APPLICANT: Orliman, Gerald
APPLICANT: Cairney, John
APPLICANT: Perrera, Ranjan
TITLE OF INVENTION: VICTLIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND
TITLE OF INVENTION: METHODS OF USING THE SAME
FILE REFERENCE: IPS/200099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACTATAGGGCACGCGGGGTCGACGGCCCGGGCTGGTCGTATTTGTGT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2%; Score 39; DB 4; Length 340; 89.4%; Pred. No. 0.098;
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Patent No. 6462257
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NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1014)...(1014)
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LOCATION: (610)...(610)
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LOCATION: (178)...(178)
NAME/KEY: unsure
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NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                     (453)...(453)
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US-09-323-195A-3
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Matches 45; Conserv
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Best Local Similarity
Matches 42; Conserv
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SOFTWARE: Pate
SEQ ID NO 3
                                                                                                                                                                                   LENGTH: 6078
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US-09-323-195A-3
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LOCATION:
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LOCATION:
NAME/KEY: L
LOCATION:
NAME/KEY: L
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TYPE: DNA
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1 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCGTATTTGTG 46
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US-09-570-367C-1/C
; Sequence 1, Application US/09570367C
; Patent No. 6338851
                                                                                                                                                                                                                                                                     Sequence 5, Application US/09424283; Patent No. 6437219; GENERAL INFORMATION:
                                                                                                                                                                            1023 AACAGCATAATTTGAAA 1007
                                                                                                                                        463 CTACGTTTGATTTGAGA 479
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity 84.3%;
Matches 43; Conservative
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4.1%;
Best Local Similarity 89.1%;
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.0
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; LOCATION: (119)...(1588)
US-09-424-283-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                  RESULT 12
US-09-424-283-5/c
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LENGTH: 1924
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APPLICANT: Heiner, Cheryl R.
APPLICANT: Leffowitz, Elliot.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 ATTTAAAGGTTAATCATTTATATTTCTAAATTATATCACATAAGATATTAATTTGATTAG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 ATTGTTAGTGAAATTATCTAGCTAACAAATAGCTACCTAACTATTAACTAATTTACCAAA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 ACTAATAGTTAGTTGGCTAAAATTGTTAGTGAAATTATCTAGCTAACAAATAGCTACCTA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 0.22;
0; Mismatches 99; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Indels
                                                                   GENERAL INFORMATION:

APPLICANT: Chiang, Vincent Lee C.

APPLICANT: Tasi, Chung-Jui

APPLICANT: Trai, Chung-Jui

APPLICANT: True of INVENTION: Genetic engineering of trees through

TITLE OF INVENTION: Manipulation of lignin biosynthesis

FILE REFERENCE: 881.003451

CURRENT APPLICATION NUMBER: US/08/969,046B

CURRENT FILING DATE: 1997-11-12

NUMBER OF SEG ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 4
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 AATACTATCGTTTTAATTAATAA 430
                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Populus tremuloides Michx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09601198
Patent No. 6531583
GENERAL INFORMATION:
APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
RESULT 10
US-08-969-046-5/c
Sequence 5, Application US/08969046B
; Patent No. 6455762
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4.2%;
Best Local Similarity 49.7%;
Matches 98; Conservative
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Best Local Similarity 54.55
Matches 78; Conservative
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343 ACTATTAACTAATTTACCAAAAATAACTTATAGTTAAATTATTAAGTTGGGCTGTTTGAA 402
                                                                                    403 TGTCTCAACTAATTTTAGCCACTAACTTTTATCTTTAGTGCATTCAAACATGGCATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Gorczynski, Reginald M.
TITLE OF INVENTION: Methods and Compositions for Immunomodulation
FILE REFERENCE: 9579-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCGTATTTGTGTCCAA 51
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Pred. No. 0.32;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 2791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Grimes, et al.
TITLE OF INVENTION: Sucrose binding proteins
FILE REPERENCE: 4630-50206
CURRENT APPLICATION NUMBER: US/09/424,283
CURRENT FILING DATE: 1999-11-19
PRIOR PLICATION NUMBER: PCT/US98/10465
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: 05 60/047,568
PRIOR FILING DATE: 1997-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 4
Pred. No. 0.43;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/570,367C CURRENT FILING DATE: 2000-05-05 PRIOR APPLICATION NUMBER: US 60/064,764 PRIOR FILING DATE: 1997-11-07
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g

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POTHER INFORMATION: Sequence CATGGGGA
FEATURE:
NAME/KEY: TF binding-site
LOCATION: 397..410
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: score 0.963
OTHER INFORMATION: sequence CTCTCGGAAGCCT
FEATURE:
NAME/KEY: TF binding-site
LOCATION: 400..409
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: score 0.974
OTHER INFORMATION: score 0.974
OTHER INFORMATION: score 0.974
INFORMATION: score 0.974
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: score 0.974
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: score 0.974
OTHER INFORMATION: score 0.974
OTHER INFORMATION: score 0.963
LOCATION: complement(193..204)
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: name USF_01
OTHER INFORMATION: score 0.985
OTHER INFORMATION: sequence CAGCACGTGAGT
                                                                                                                                                  FEATURE:
NAME/KEY: TF binding-site
LOCATION: complement(193..204)
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: score 0.956
OTHER INFORMATION: sequence CAGCACGTGAGT
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: complement(193..204)
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: name MYCMAX_02
OTHER INFORMATION: score 0.972
OTHER INFORMATION: sequence CAGCACGTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 195.202
IDENTIFICATION METHOD: matinspector prediction OTHER INFORMATION: name USF_C
OTHER INFORMATION: score 0.997
OTHER INFORMATION: sequence TCACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: TF binding-site
LOCATION: complement(195...202)
LDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: name USF_C
OTHER INFORMATION: score 0.991
OTHER INFORMATION: sequence GCACGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: TF binding-site
LOCATION: complement(210.217)
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: name MET. 01
OTHER INFORMATION: secue 0.968
OTHER INFORMATION: sequence CATGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: TF binding-site
LOCATION: complement(460..470)
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: name APIEJ_Q2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: TF binding-site
LOCATION: 547.555
IDENTIFICATION METHOD: matinspector prediction
OTHER INFORMATION: name PADS_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence AGTGACTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: TF binding-site
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us-10-039-836a-3.rni

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Score 37.8; DB 4;
Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: score 0.991
OTHER INFORMATION: score 0.991
OTHER INFORMATION: sequence gcacgtga
FEATURE:
NAME/KEY: protein_bind
LOCATION: complement(210..217)
OTHER INFORMATION: mame MZFL_01
OTHER INFORMATION: mame MZFL_01
OTHER INFORMATION: score 0.968
OTHER INFORMATION: sequence catgggga
FEATURE:
NAME/KEY: protein_bind
LOCATION: 397..410
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: sequence ctcccggaagcct
FEATURE:
NAME/KEY: protein_bind
OTHER INFORMATION: sequence ctcccggaagcct
FEATURE:
NAME/KEY: protein_bind
LOCATION: 409.
                                                              OTHER INFORMATION: matinspector prediction OTHER INFORMATION: name NMYC_01 OTHER INFORMATION: score 0.956 OTHER INFORMATION: sequence cagcacgtgagt
                                                                                                                                                                     FEATURE:
NAME/KEY: protein bind
LOCATION: complement(193..204)
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: name MYCMAX_02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 400..409

CTHER INFORMATION: matinspector prediction OTHER INFORMATION: name CETS1D54_01

OTHER INFORMATION: score 0.974

OTHER INFORMATION: sequence tccggaagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: protein_bind
LOCATION: conplement(460..470)
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: name API_Q4
OTHER INFORMATION: score 0.963
OTHER INFORMATION: sequence agtgactgaac
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: protein_bind
COCATION: 195..202
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: name USF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: protein_bind
LOCATION: complement(195..202)
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: name USF_C
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NAME/KEY: protein_bind
LOCATION: complement(460..470)
OTHER INFORMATION: matinspector prediction
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JOCATION: 547..555

OTHER INFORMATION: mate PADS_C
OTHER INFORMATION: name PADS_C
OTHER INFORMATION: score 1.000

OTHER INFORMATION: sequence tgtggtctc
US-09-247-155-37
                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: score 0.972
OTHER INFORMATION: sequence cagcacgtgagt
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OTHER INFORMATION: score 0.961
OTHER INFORMATION: sequence agtgactgaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: score 0.997
OTHER INFORMATION: sequence tcacgtgc
                                             complement(193..204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    name USF_C
score 0.997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              name USF_C
score 0.991
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86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                        ö
                                                                                                                                                                           Gaps
                                                                                                                                                                        ö
                                                                                                            Ouery Match 4.1%; Score 37.8; DB 3; Length 555; Best Local Similarity 86.7%; Pred. No. 0.26; Matches 39; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                               2 CTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCGTATTTGTG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET. O21A
CURRENT APPLICATION NUMBER: 60/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER PILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER PILING DATE: 1998-04-13
EARLIER PILING DATE: 1998-04-13
EARLIER PILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-10
SOFTWARE: PAPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER: PAPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER: PAPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: SCOLE 0.304
OTHER INFORMATION: Sequence ggactcacgtgctgct
FEATURE:
NAME/KEY: protein_bind
LOCATION: 193..204
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: score 0.965
OTHER INFORMATION: Sequence actcacgtgctg
FEATURE:
NAME/KEY: protein_bind
LOCATION: 193..204
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: sequence actcacgtgctg
OTHER INFORMATION: sequence actcacgtgctg
FEATURE:
OTHER INFORMATION: sequence actcacgtgctg
FEATURE:
NAME/KEY: protein_bind
FEATURE:
NAME/FEY: protein_bind
InAME/FEY: protein_bind
InAME/FEY: protein_bind
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LOCATION: 191..206
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: name ARNT_01
OTHER INFORMATION: score 0.964
OTHER INFORMATION: score 1.000 OTHER INFORMATION: sequence TGTGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCATION: complement(193..204)
OTHER INFORMATION: matinspector prediction
OTHER INFORMATION: name USF_01
OTHER INFORMATION: score 0.985
OTHER INFORMATION: sequence cagcacqtgagt
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: codon_start="501"
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09247155A
Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEC ID NO 37
LENGTH: 555
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: promoter LOCATION: 1..500 FEATURE:
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US-09-247-155-37
                                                      US-08-905-223-37
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Length 555;

0;			
0; Gaps			
0;			
4; Indels	TCGTATTTGTG 46	TCTGGTCTGTK 45	
2; Mismatches	SGCCCGGGCTGG	GGCCCGGGCTGG	10:50:08
2;	CGAC	rcgac	03,
39; Conservative	2 CTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCGTATTTGTG 46	1 CTATAGGCACGCKTGGTCGACGGCCCGGGCTGGTCTGGTC	Search completed: October 17, 2003, 10:50:08
39;	2 CT	1 4	leted
Matches	Qy	QQ	Search comp

Job time : 67 secs